

SEQUENCE LISTING

<110> Irie, Reiko
 Tsunoda, Hiroyuki
 Igawa, Tomoyuki
 Sekimori, Yasuo
 Tsuchiya, Masayuki

<120> IgM PRODUCTION BY TRANSFORMED CELL AND
 METHOD OF QUANTIFYING THE SAME

<130> 14875-155US1

<150> PCT/JP2004/010444
 <151> 2004-07-15

<150> US 60/487,333
 <151> 2003-07-15

<160> 31

<170> PatentIn version 3.1

<210> 1
 <211> 1779
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> (1)..(1779)

<400> 1		
atg gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt		48
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly		
1 5 10 15		
gtc cag tgt gag gtc cag ctg ttg gat tct ggg gga ggc ttg gta cag		96
Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Leu Val Gln		
20 25 30		
cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt		144
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe		
35 40 45		
agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg		192
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu		
50 55 60		
gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca		240
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala		
65 70 75 80		
gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac		288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn		
85 90 95		

acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta		336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val		
100	105	110
tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct		384
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala		
115	120	125
tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc		432
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala		
130	135	140
cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat acg		480
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr		
145	150	155
165	170	175
528		
agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc		
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser		
165	170	175
atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc		576
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr		
180	185	190
624		
cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca		
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser		
195	200	205
210	215	220
672		
cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac		
Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His		
210	215	220
225	230	235
240		
720		
gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg		
Val Val Cys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val		
225	230	235
240		
768		
cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc		
Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val		
245	250	255
816		
cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc		
Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile		
260	265	270
270		
864		
tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg		
Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu		
275	280	285
285		
912		
cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag		
Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln		
290	295	300
300		
960		
gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca		
Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr		
305	310	315
320		

ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys 325 330 335	1008
cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met 340 345 350	1056
tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro 355 360 365	1104
tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu 370 375 380	1152
gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg 385 390 395 400	1200
cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His 405 410 415	1248
ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp 420 425 430	1296
gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp 435 440 445	1344
ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala 450 455 460	1392
ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu 465 470 475 480	1440
aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser 485 490 495	1488
ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser 500 505 510	1536
ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro 515 520 525	1584
ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp 530 535 540	1632
aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc	1680

Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro			
545	550	555	560
aac agg gtc acc gag agg acc gtc gac aag tcc acc ggt aaa ccc acc			1728
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr			
565	570	575	
ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac			1776
Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr			
580	585	590	
tga			1779
<210> 2			
<211> 592			
<212> PRT			
<213> Homo sapiens			
<400> 2			
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly			
1	5	10	15
Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln			
20	25	30	
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe			
35	40	45	
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
50	55	60	
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala			
65	70	75	80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn			
85	90	95	
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val			
100	105	110	
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala			
115	120	125	
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala			
130	135	140	
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr			
145	150	155	160
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser			
165	170	175	
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr			
180	185	190	
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser			
195	200	205	

Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
 210 215 220

Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
 225 230 235 240

Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
 245 250 255

Pro Pro Arg Asp Gly Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
 260 265 270

Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
 275 280 285

Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
 290 295 300

Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
 305 310 315 320

Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
 325 330 335

Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
 340 345 350

Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
 355 360 365

Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
 370 375 380

Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
 385 390 395 400

Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
 405 410 415

Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
 420 425 430

Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
 435 440 445

Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
 450 455 460

Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
 465 470 475 480

Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
 485 490 495

Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
 500 505 510

Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
 515 520 525

Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
 530 535 540

Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
 545 550 555 560

Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
 565 570 575

Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
 580 585 590

<210> 3

<211> 723

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(723)

<400> 3

atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct
 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct
 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
 35 40 45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag
 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60

aaa cca gga cag cct aag ctg ctc att tac tgg gca tct acc cgg
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95

ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
 100 105 110

tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc
 Tyr Cys Gln Gln Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr

115	120	125	
aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe			432
130	135	140	
ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys			480
145	150	155	160
ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val			528
165	170	175	
gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln			576
180	185	190	
gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser			624
195	200	205	
aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His			672
210	215	220	
cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			720
225	230	235	240
tag			723
<210> 4			
<211> 240			
<212> PRT			
<213> Homo sapiens			
<400> 4			
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser			
1	5	10	15
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala			
20	25	30	
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser			
35	40	45	
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln			
50	55	60	
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg			
65	70	75	80
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp			
85	90	95	
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr			

100

105

110

Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
 115 120 125

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
 130 135 140

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 145 150 155 160

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 165 170 175

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 180 185 190

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 195 200 205

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 210 215 220

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235 240

<210> 5

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(480)

<400> 5

atg aag aac cat ttg ctt ttc tgg gga gtc ctg gcg gtt ttt att aag 48
 Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys
 1 5 10 15

gct gtt cat gtg aaa gcc caa gaa gat gaa agg att gtt ctt gtt gac 96
 Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
 20 25 30

aac aaa tgt aag tgt gcc cgg att act tcc agg atc atc cgt tct tcc 144
 Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
 35 40 45

gaa gat cct aat gag gac att gtg gag aga aac atc cga att att gtt 192
 Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val
 50 55 60

cct ctg aac aac agg gag aat atc tct gat ccc acc tca cca ttg aga 240
 Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
 65 70 75 80

acc aga ttt gtg tac cat ttg tct gac ctc tgt aaa aaa tgt gat cct	288
Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro	
85 90 95	
aca gaa gtg gag ctg gat aat cag ata gtt act gct acc cag agc aat	336
Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn	
100 105 110	
atc tgt gat gaa gac agt gct aca gag acc tgc tac act tat gac aga	384
Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg	
115 120 125	
aac aag tgc tac aca gct gtg gtc cca ctc gta tat ggt ggt gag acc	432
Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr	
130 135 140	
aaa atg gtg gaa aca gcc tta acc cca gat gcc tgc tat cct gac taa	480
Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp	
145 150 155	
<210> 6	
<211> 159	
<212> PRT	
<213> Homo sapiens	
<400> 6	
Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys	
1 5 10 15	
Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp	
20 25 30	
Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser	
35 40 45	
Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val	
50 55 60	
Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg	
65 70 75 80	
Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro	
85 90 95	
Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn	
100 105 110	
Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg	
115 120 125	
Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr	
130 135 140	
Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp	
145 150 155	
<210> 7	

```

<211> 24
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized sequence

<400> 7
ccaacggcaa caaagaaaaag aacg                                24

<210> 8
<211> 24
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized sequence

<400> 8
aacatgctct ggccgagcca gtcg                                24

<210> 9
<211> 24
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized sequence

<400> 9
gcaagtccag ccagagtgtt ttat                                24

<210> 10
<211> 24
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized sequence

<400> 10
ctgtccttgc tgtcctgctc tgtg                                24

<210> 11
<211> 33
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 11
aacagctcga gccaccatgg agtttgggct gag                                33

<210> 12
<211> 32
<212> DNA

```

<213> Artificial		
<220>		
<223> an artificially synthesized primer sequence		
<400> 12		
agcggccagc cgcccccagc ctgtcgacag gc		32
<210> 13		
<211> 32		
<212> DNA		
<213> Artificial		
<220>		
<223> an artificially synthesized primer sequence		
<400> 13		
atagaattcc accatggtgt tgcagaccca gg		32
<210> 14		
<211> 30		
<212> DNA		
<213> Artificial		
<220>		
<223> an artificially synthesized primer sequence		
<400> 14		
ggagcaggcg gccgcacttc tccctctaac		30
<210> 15		
<211> 24		
<212> DNA		
<213> Artificial		
<220>		
<223> an artificially synthesized sequence		
<400> 15		
accattgaga accagatttg tgta		24
<210> 16		
<211> 24		
<212> DNA		
<213> Artificial		
<220>		
<223> an artificially synthesized sequence		
<400> 16		
tgtgtacac ttgtttctgt cata		24
<210> 17		
<211> 28		
<212> DNA		
<213> Artificial		

<220>
 <223> an artificially synthesized primer sequence

<400> 17
 atgaattcca ccatgaagaa ccatttgc 28

<210> 18
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 18
 tatcttagatt agtcaggata gcaggc 26

<210> 19
 <211> 1788
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1788)

<400> 19
 atg gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt 48
 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
 1 5 10 15

gtc cag tgt gag gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag 96
 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Leu Val Gln
 20 25 30

ccg ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

agc agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192
 Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60

gag tgg gtc tca gct att agt ggt tat acc aca tac tac gca 240
 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Tyr Thr Thr Tyr Tyr Ala
 65 70 75 80

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac 288
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 85 90 95

acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta 336
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 100 105 110

tat tac tgt gcc aaa aaa ccg ggg gac tat ggt tcg ggg agt tat tac 384

Tyr	Tyr	Cys	Ala	Lys	Lys	Pro	Gly	Asp	Tyr	Gly	Ser	Gly	Ser	Tyr	Tyr	
115						120						125				
ctt	gac	tac	tgg	ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca	ggg	agt	432
Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Ser	
130						135						140				
gca	tcc	gcc	cca	acc	ctt	ttc	ccc	ctc	gtc	tcc	tgt	gag	aat	tcc	ccg	480
Ala	Ser	Ala	Pro	Thr	Leu	Phe	Pro	Leu	Val	Ser	Cys	Glu	Asn	Ser	Pro	
145						150					155			160		
tcg	gat	acg	agc	agc	gtg	gcc	gtt	ggc	tgc	ctc	gca	cag	gac	ttc	ctt	528
Ser	Asp	Thr	Ser	Ser	Val	Ala	Val	Gly	Cys	Leu	Ala	Gln	Asp	Phe	Leu	
165						170					175					
ccc	gac	tcc	atc	act	ttc	tcc	tgg	aaa	tac	aag	aac	aac	tct	gac	atc	576
Pro	Asp	Ser	Ile	Thr	Phe	Ser	Trp		Lys	Tyr	Lys	Asn	Asn	Ser	Asp	Ile
180						185					190					
agc	agc	acc	cgg	ggc	ttc	cca	tca	gtc	ctg	aga	ggg	ggc	aag	tac	gca	624
Ser	Ser	Thr	Arg	Gly	Phe	Pro	Ser	Val	Leu	Arg	Gly	Gly	Lys	Tyr	Ala	
195						200					205					
gcc	acc	tca	cag	gtg	ctg	ctg	cct	tcc	aag	gac	gtc	atg	cag	ggc	aca	672
Ala	Thr	Ser	Gln	Val	Leu	Leu	Pro	Ser	Lys	Asp	Val	Met	Gln	Gly	Thr	
210						215					220					
gac	gaa	cac	gtg	gtg	tgc	aaa	gtc	cag	cac	ccc	aac	ggc	aac	aaa	gaa	720
Asp	Glu	His	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn	Lys	Glu	
225						230					235			240		
aag	aac	gtg	cct	ttt	cca	gtg	att	gtc	gag	ctg	cct	ccc	aaa	gtg	agc	768
Lys	Asn	Val	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys	Val	Ser	
245						250					255					
gtc	tcc	gtc	cca	ccc	cgc	gac	ggc	ttc	ttc	ggc	aac	ccc	cgc	aag	tcc	816
Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg	Lys	Ser	
260						265					270					
aag	ctc	atc	tgc	cag	gcc	acg	ggt	ttc	agt	ccc	cgg	cag	att	cag	gtg	864
Lys	Leu	Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln	Ile	Gln	Val	
275						280					285					
tcc	tgg	ctg	cgc	gag	ggg	aag	cag	gtg	ggg	tct	ggc	gtc	acc	acg	gac	912
Ser	Trp	Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val	Thr	Thr	Asp	
290						295					300					
cag	gtg	cag	gct	gag	gcc	aaa	gag	tct	ggg	ccc	acg	acc	tac	aag	gtg	960
Gln	Val	Gln	Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr	Tyr	Lys	Val	
305						310					315			320		
acc	agc	aca	ctg	acc	atc	aaa	gag	agc	gac	tgg	ctc	agc	cag	agc	atg	1008
Thr	Ser	Thr	Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Ser	Gln	Ser	Met	
325						330					335					
ttc	acc	tgc	cgc	gtg	gat	cac	agg	ggc	ctg	acc	ttc	cag	cag	aat	gcg	1056
Phe	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Gln	Gln	Asn	Ala	

340	345	350	
tcc tcc atg tgt gtc ccc gat caa gac aca gcc atc cg ^g gtc ttc gcc Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala			1104
355	360	365	
atc ccc cca tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu			1152
370	375	380	
acc tgc ctg gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc Thr Cys Leu Val Thr Asp Leu Thr Tyr Asp Ser Val Thr Ile Ser			1200
385	390	395	400
tgg acc cgc cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser			1248
405	410	415	
gag agc cac ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile			1296
420	425	430	
tgc gag gat gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr			1344
435	440	445	
cac aca gac ctg ccc tcg cca ctg aag cag acc atc tcc cg ^g ccc aag His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys			1392
450	455	460	
ggg gtg gcc ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cg ^g Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg			1440
465	470	475	480
gag cag ctg aac ctg cg ^g gag tcg gcc acc atc acg tgc ctg gtg acg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr			1488
485	490	495	
ggc ttc tct ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln			1536
500	505	510	
ccc ttg tcc ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro			1584
515	520	525	
cag gcc cca ggc cg ^g tac ttc gcc cac agc atc ctg acc gtg tcc gaa Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu			1632
530	535	540	
gag gaa tgg aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu			1680
545	550	555	560
gcc ctg ccc aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly			1728
565	570	575	

aaa ccc acc ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc	1776
Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly	
580 585 590	
acc tgc tac tga	1788
Thr Cys Tyr	
595	
<210> 20	
<211> 595	
<212> PRT	
<213> Homo sapiens	
<400> 20	
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly	
1 5 10 15	
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln	
20 25 30	
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
35 40 45	
Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Tyr Thr Thr Tyr Tyr Ala	
65 70 75 80	
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn	
85 90 95	
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val	
100 105 110	
Tyr Tyr Cys Ala Lys Lys Pro Gly Asp Tyr Gly Ser Gly Ser Tyr Tyr	
115 120 125	
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser	
130 135 140	
Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro	
145 150 155 160	
Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu	
165 170 175	
Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile	
180 185 190	
Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala	
195 200 205	
Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr	
210 215 220	

Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu
 225 230 235 240

Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser
 245 250 255

Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser
 260 265 270

Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val
 275 280 285

Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp
 290 295 300

Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val
 305 310 315 320

Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser Gln Ser Met
 325 330 335

Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala
 340 345 350

Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala
 355 360 365

Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu
 370 375 380

Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser
 385 390 395 400

Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser
 405 410 415

Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile
 420 425 430

Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr
 435 440 445

His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys
 450 455 460

Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg
 465 470 475 480

Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr
 485 490 495

Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln
 500 505 510

Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro
 515 520 525

Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu
530 535 540

Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu
545 550 555 560

Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly
565 570 575

Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly
580 585 590

Thr Cys Tyr
595

<210> 21
<211> 726
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (1)..(726)

<400> 21
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

```

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20          25          30

```

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
 35 40 45

```

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
      50          55          60

```

```

aaa cca gga cag cct cct aag ttg ctc att tac tgg gca tct acc cg
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65          70          75          80

```

```

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85          90          95

```

```

ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100          105          110

```

tac tgt cag caa tat tat act act ctt ccg ctc act ttc ggc gga ggg 384
 Tyr Cys Gln Gln Tyr Tyr Thr Thr Leu Pro Leu Thr Phe Gly Gly Gly
 115 120 125

acc aag gtg gag atc aaa cga act gtg gct gca cca tct gtc ttc atc	432
Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile	
130 135 140	
ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg	480
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val	
145 150 155 160	
tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag	528
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys	
165 170 175	
gtg gat aac gcc ctccaa tcg ggt aac tcc cag gag agt gtc aca gag	576
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu	
180 185 190	
cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg	624
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu	
195 200 205	
agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc	672
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr	
210 215 220	
cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag	720
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu	
225 230 235 240	
tgt tag	726
Cys	

<210> 22	
<211> 241	
<212> PRT	
<213> Homo sapiens	
<400> 22	
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala	
20 25 30	
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser	
35 40 45	
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln	
50 55 60	
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg	
65 70 75 80	
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
85 90 95	

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
 100 105 110
 Tyr Cys Gln Gln Tyr Tyr Thr Thr Leu Pro Leu Thr Phe Gly Gly Gly
 115 120 125
 Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
 130 135 140
 Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
 145 150 155 160
 Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
 165 170 175
 Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
 180 185 190
 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
 195 200 205
 Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
 210 215 220
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
 225 230 235 240

Cys

<210> 23
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> an artificially synthesized primer sequence

 <400> 23
 caacaggcag gcaggggcag caag 24

 <210> 24
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> an artificially synthesized primer sequence

 <400> 24
 agcataatta aagccaaagga ggag 24

 <210> 25
 <211> 68
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized sequence

<400> 25
 cctgatcatg aagacgtcga ctagtccgga tccccgggag ctcgagcgct ctagatctt 60
 aattaagg 68

<210> 26
 <211> 76
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized sequence

<400> 26
 cgccgccttaa ttaaagatct agagcgctcg agctccggg gatccggact agtcgacgtc 60
 ttcatgatca ggccgg 76

<210> 27
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 27
 gaggaaattcc accatgaaga acc 23

<210> 28
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 28
 gaggcggccg cttagtcagg atagcag 27

<210> 29
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 29
 aaaagcggcc gcgatcataa tcagccatac ca 32

<210> 30
 <211> 36
 <212> DNA

<213> Artificial
<220>
<223> an artificially synthesized primer sequence

<400> 30
aaaactcgag aagcttagac atgataagat acattg 36

<210> 31
<211> 12
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized linker sequence

<400> 31
cccgatccg gg 12